

REMARKS

Claims 1-15 are pending.


The specification has been amended for to give proper reference to all sequences in substitute Sequence Listing filed herewith. No new matter is believed to be introduced by the amendment to the claims.

Applicants have now submitted a substitute Sequence Listing and a corresponding computer-readable Sequence Listing, and an amendment. Contents of the paper copy of the substitute Sequence Listing and the computer-readable Sequence Listing are identical. Support for all the sequences listed in the substitute Sequence Listing can be found in the present application. No new matter is introduced by the submission of the substitute Sequence Listing and the computer-readable Sequence Listing.

Applicants submit that this application is now in condition for examination on the merits. Early notice to this effect is earnestly solicited.

Respectfully submitted,

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**Marked-Up Copy**  
Serial No: 09/831,907  
Amendment Filed on:  
HEREWITH

IN THE SPECIFICATION

Please amend the specification as follows:

Please replace the paragraph at page 2, prenumbered lines 28-37, as follows:

--A subject of the present invention is polypeptides, isolated from mammals, characterized in that they comprise, at their C-terminal end, a heptapeptide having the following sequence: Cys-Phe, Trp-Lys-Tyr-Cys-Xaa (SEQ ID NO. 45), in which Xaa represents Val or Ile, in that they belong to the urotensin II family and in that they exhibit at least 45%, and preferably at least 70%, similarity with the polypeptide sequence SEQ ID NO:1, corresponding to human preprourotensin II.--

Please replace the paragraph at page 10, prenumbered line 32 to page 11, prenumbered line 2, as follows:

-- - Figure 1 illustrates the alignment of the deduced amino acid sequences of, respectively, human, frog (SEQ ID NO. 46) and carp prepro-UII (SEQ ID NOS. 47 and 48). In this figure, the signal sequence is indicated in italics; the conserved amino acids are indicated in black; the cleavage sites of the prohormone are indicated by stars and the conserved amino acid residues are indicated by a black circle. The disulfide bridge present in

the UII sequence is indicated under the urotensin II sequence. The amino acids are numbered on the right of the figure;--

Please replace the paragraph at page 11, prenumbered lines 32-37, as follows:

-- - Figure 6 is a comparison of the primary structures of urotensin II from various species (SEQ ID NOS. 49-64). Dashes have been inserted in order for the sequences to be optimally aligned. The dots illustrate the amino acids residues which are identical between the various sequences, with respect to the human sequence;--